

FIGURE 1

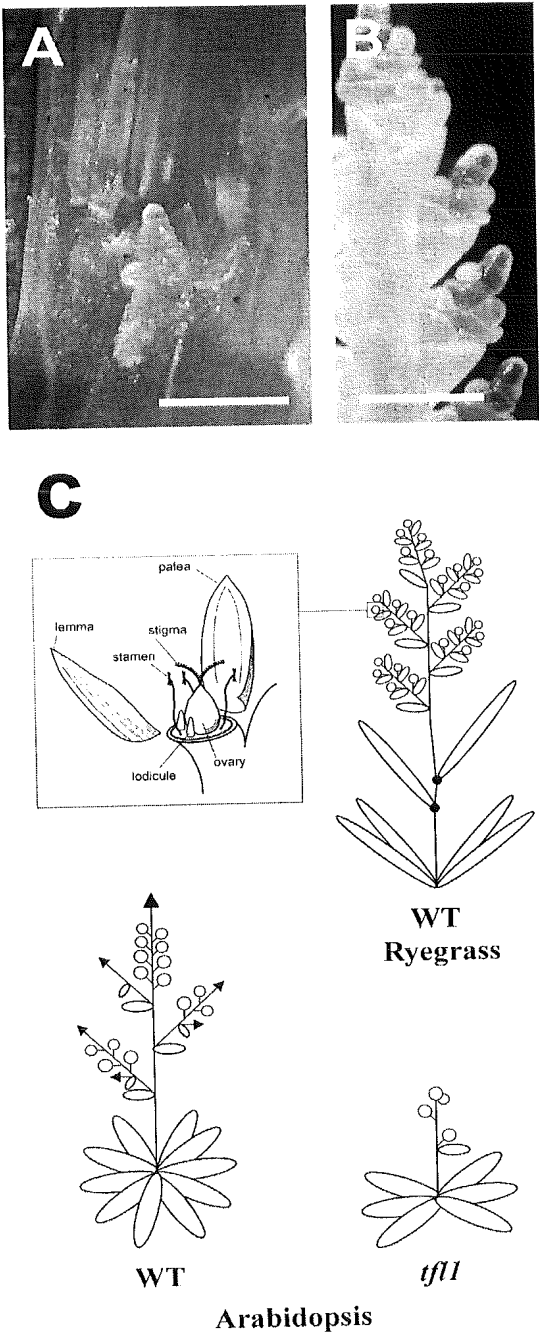


FIGURE 2

		GCC	-76
-75	CAAGCCACTTCAAAGCTTTGCTACTACCAGATAGAGCATTCACCGTGCAATATAGAAATACTTGCCTCTCCAACC	-1	
1	ATGTCTAGGTCTGTGGAGCCTCTTATTTGTTGGTCGTGTTCATTTGGAGAAGTTCTCGATCCATTTAACCCTGTGTG	75	
76	AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCATCAGCAGTTGTATCT	150	
151	AAACCAAGAGTAGAGGTTTCAAGGGGGTGACTTGGCGATCCTTATTCACATTTGGTTATGACGGACCCAGATGTGCCA	225	
226	GGACCAAGTGATCCGTATCTGCGGGAGCATCTTCACTGGATTTGTCAGTAATATACCTGGGACAACAGATGCTTCA	300	
301	TTTGGGGGGGAGGTCATGAGCTATGAGAGCCCAAAGCCCAACATTTGGAATCCACAGGTTTCAATTTTGTGCTCTTC	375	
375	AAGCAGAAGCGAAGGCAGACTGTATCTGTGCCTTCCTTCAGGGATCATTTCAACACCCGCCAGTTTGTGTGGAT	450	
451	AATGATCTTTGGCCTCCCTGTGGCTGCTGTTTACTTCAATTTGTCAGAGAGAGACTGCTGCCAGGAGGCGCTGAAAA	525	
526	TCGAGTTCTTTGGCTATCCAGTTGTGCCAAATAAAGGCTTTTGGAGTTATGCACCTTCTTTCTGAAGTCAATGCT	600	
601	CCTCTTCTACATTACTTCCTCGTGGACCATTGCTTCTTTACTACAGTTTTTGTCTCAGGGATCAAATAAATCAAGT	675	
675	GCATTTTGGAGATTGTATTTAGATTATATTGTAAGCAGTGAGATCAGCAACCATGTGTTAACATAAGCCAGTACAT	750	
751	TAGCAGGTCCATGTTTATGGTTTCATGTTGTGTGTAAGCAGTTATCACTAGAAGGAAGGTGAGGTAGACAACCCA	825	
826	AAC TG GCAAAAAAAAAAGCTTTATCTA	851	

FIGURE 3A

-3600	cactagtaacggccgcagtgctggaattcagggtaatacgcactcactatagggmgctcgaggatcttcccac	-3526
-3525	cagtgtgcattcatgtgttacttaccactctccaacttgagggactcaagattgggtgggggctccttttcgctg	-3451
-3450	aagcgatccaaagggtgtcgggtaacgggttatgcacagcaaacagaaaacatcgccatctgcacggaagccagaagt	-3376
-3375	agttactatgtcaaagggatataaaaaactcactaatgaagggggatgctattgctgagataaaactgctatctca	-3301
-3300	tctacaggtgagattgcaagtatacttgacaacagggccagatgggatggcatgaagaaaattagggctggagta	-3226
-3225	gaaaggtaagatatgcatggatttggatgagatggcttagagggttgcgagatatcaaatagaagacacttcttca	-3151
-3150	atgattcaatagaagatgcatgtgccattacagagtggattattatgtcctttttaagagatgcttacgtccct	-3076
-3075	gacctttctataacacaattacactcctttgctagacttttccctgctataattgtctttccctcgccaaaagaat	-3001
-3000	aatactatagaacttccataatttaatttcccccttattttcttggactctatcttaattctcctcctattgttcag	-2926
-2925	ccaaggactgctccttccatttacttgccgccacgggctgactgacaatgacacctgcgcgctttgtgatcaagag	-2851
-2850	cctgaatctattttcactcatgctgcaatgctccttctcacagcaaatatgggatgatatctgcagtaagctc	-2776
-2775	aacctttctgccatgtagccagttggcaacgcgcagttcagcatttgggtcgcgcgagctgccgccaacgctcaa	-2701
-2700	ccagccctgcagaaggggtgctaaatccatcatcatccttactctctggagattatggaagacgaggaacgatgct	-2626
-2625	atcttcaaaaatctggcccccacagactcgccttagttcagtcgactcctagatgaagcctgtcaatggctcgtta	-2551
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-2400	tttggtagcttttctactcttgtatgctcccgctcttctcgcagcgttcttcttaatatataatgacgcagtctt	-2326
-2325	gcatgtgttcgagaaaaaaatttacttacctcttaggctatattctcttcccaacttggactccacaagcttc	-2251
-2250	aatcgcaacttgtccaagctgctgcgcgtgggtgctgctgctccttttccaatgcatccatacactgtcctagtcag	-2176
-2175	cataccaacaaaaaagctaatgccgcccctgttgtttcaaatgaattatctgattgtgatgctgctaactcttt	-2101
-2100	gcatatgagctcgcggcatatgaatgaacttgggttggcagaatgaacaagagaggacttcttgatggatatag	-2026
-2025	cactggtaagctgaagttctgtgagcaggctatgatgttccctgttaaaaaaaggctatgaaaaacttgtgat	-1951
-1950	agggtgtaagtatgtgttttattttgcgtgcaaattgggatgcatggaaagtgtgtagtgctactagctgtgtgtg	-1876
-1875	ctactgtgctaccaacacactgtagcactgccccaaaatttatgaaaaagctctgaacagacgagatgtatctatca	-1801
-1800	attcatggaccatttttgttataattttcttttaaaataaaaaattccgtaaagaatcaataagtggaattattg	-1726
-1725	gaaatgaaaaaagtaaccaaaataactaaactttttttcaaatacagatcggatatcatggagacacactggctac	-1651
-1650	catgtgttggatatgctactagattccactacagctagggtgtcaagcaactataatggcatcagaatggagcaga	-1576
-1575	aaaatgtcacaaagctgtacttcaactccactacttctagctgcacaaatgtcaagcaggcatgattgcactagacc	-1501
-1500	agaacatagtaaatgcataaagctgtaattggctccactacttatggaaacgaagaaatctattattttattgtttt	-1426
-1425	aatcgagatgaagctgtgataattttatcgctgaaatgacatttcagcactagacagcaccttagacaattaaagt	-1351
-1350	gggtgggtgactgtattccatttctttattctcttccatgggtgtgttcccatagtactacaagaagagaataaa	-1276
-1275	cagataataatggtaatgcacttgggtatcgaaagttttaggaaagattctaattctagagcaattgaactcaaca	-1201
-1200	acaacttcccttttcttaacagaaaaagaatcgggtcaaacgaggcttgcttaaaccaaacactataaagacg	-1126
-1125	aacatttgaggggtgaagaggcttccacgtggacagtgccgcagtggttctgtccactagataaacacctaaataata	-1051
-1050	gttaaaaaacaagaggataagaatatcagaaaagccagaccttaaatttctgcaagcaaacatcaaatgaagtatg	-976
-975	caaaaaacgaattgatagtttaggaaagcatcactccaaagtgttttattcccgcttctttttcatttgcctccaca	-901
-900	gggcatacttccataaatttctgcgaacaattacatctagatctttttaaactgaagtatttttagcatgaaaacg	-826
-825	catgttctgtaatgtggctgtgaatttcggactgctcatctgatttccctctggtagaatacataaataattat	-751
-750	acacaacagcatgataatgtgcaaaactaagcatcaaatctgcacattgtcatgcagaaactaggacaggagga	-676
-675	ccagcactttgtcgtttgccttaaccaatattaacatagttcagcaacataaatcttcagagaccactagcatga	-601
-600	agggtgtgttatgtttcctaaagaaataacatgtaggtagtgatcacaataccttttttggggactataagggtg	-526
-525	gaaacctcaacttgaaaagggttccattttaatcaagtaaaaaaacagtattttttaactatcaataactaaaa	-451
-450	ttaaaacagaatagagatatactaacaatgaaaatcaaacagttgtgcaaatgtatattatcgtagtttagtatct	-376
-375	catgtttctggtgaaaaaattctctgcccctagaacttgggaagaagatgcatgaagtattactccaaactccaac	-301
-300	actgtgcaactgatagaaaagaacaagacccttgggtggctgtctcggaaaaagtgggttaggtcctttctgtgg	-226
-225	ccttttcagttctttccacgcatacccaacaaaaaagaacacagatactactcatgtctcacattctcttttga	-151
-150	gcttacactcgaagcaggcttcttgccctcataagtagaggctcgctgactctagcaatgctcagtaagcaGCC	-76
-75	CAAGCCACTTCAAAGCTTTGCTACTACCAGATAGAGCATTCACCGTGCAATATAGAAATACTTGCCTCTCCAACC	-1
1	ATGTCTAGGTCTGTGGAGCCTCTTATTGTTGGTGTGTCATTGGAGAAGTTCTCGATCCATTTAACCCATGTGTG	75
76	AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCATCAGCAGTTGTATCT	150
151	AAACCAAGAGTAGAGGTTCAAGGGGGTGACTTGCATCCTTATTCACATTGgtagaatgcactcgactcgactcct	225
226	ggaactccatattcaacttcagagtattgtatgctgtgtttctcttcttcgcagtgccataattatctcatatttca	300
301	gGTTATGACGGACCCAGATGTGCCAGGACCAAGTGATCCGTATCTGCGGGAGCATCTTCACTGGtaacctttctc	375
375	atgcacagttttttctgctgggtggctactaagcacctaaatatattagtatatttttttgaaaggaaaatatat	450

FIGURE 3B

451	tagtatatgttgctaaggaatatagaagtacatcttcttcttgcacatatatagacagagagactattttaatag	525
526	cacttctaacgagagtcatttaccaataccttttacacttacacaggATTGTCAGTAATATACCTGGGACAACAG	600
601	ATGCTTCATTTGGtaggtccttctctgagatttgaattggtatatcttatgttctgcattttgaatgaataacca	675
675	ctgaccttttgaattgcaggGGGGGAGGTCATGAGCTATGAGAGCCCAAAGCCCAACATTGGAATCCACAGGTTTC	750
751	ATTTTTGTGCTCTTCAAGCAGAAGCGAAGGCAGACTGTATCTGTGCCTTCCTTCAGGGATCATTTCAACACCCGC	825
826	CAGTTTGTGCTGTGGATAATGATCTTGGCCTCCCTGTGGCTGCTGTTTACTTCAATTGTGAGAGAGACTGCTGCC	900
901	AGGAGGCGCTGAAAATCGAGTTCTTGGCTATCCAGTTGTGCCAAATAAAGGCTTTGGAGTTATGCACCTTCTT	975
976	TCTGAAGTCAATGCTCCTCTTCTACATTACTTCTCGTGGACCATTGCTTCTTTACTACAGTTTTTGCTCAGGGA	1050
1051	TCAAATAAATCAAGTGCATTTTGGAGATTGTATTAGATTATATTGTAAGCAGTGAGATCAGCAACCATGTGTAA	1125
1126	CATAAGCCAGTACATTAGCAGGTCCATGTTTATGGTTTCATGTTGTGTAAGCAGTTATCACTAGAAGGAAGGT	1200
1201	CAGGTAGACAACCCAACTGGCAAAAAAAAAAGCTTTATCTActgtatggcccttgccggcttgatgttccatgc	1275
1276	accttttctgacatgctgtctactgtatgccaccgccactataatgtatgagatatgaatataaaatggagatat	1350
1351	ccaaaatatccagatgattgcccactaaatgctaaatgtacatagtggttttccacctattttgacttccatcat	1425
1426	gtccttacacaaaatcagaaaacatccatttcatgcacattgatgcacactgcatattaacaatctattcagatt	1500
1501	tggctgtaaacacacccttattttccgcatccattaatattatattagtagccctggacaggttaagcttttgcag	1575
1576	cacagtaagtaaccgatgaaattacaatatgatcctcgagcgccctat	1624

FIGURE 4

1	MSRSVEPLIVGRVIGEVLDPFNPCKVMVATYNSNKLVFNGHELYPYSAVSVKPRVEVQGGDLRSLFTLVMTDPDVP	75
76	GPSDPYLRHLHWIVSNIPGTTDASFGGEVMSYESPKPNIGIHRFIFVLFKQKRRQTVSVPSFRDHFNTRQFAVD	150
151	NDLGLPVAAVYFNCQRETAARRR	173

REPLACEMENT SHEET

FIGURE 5

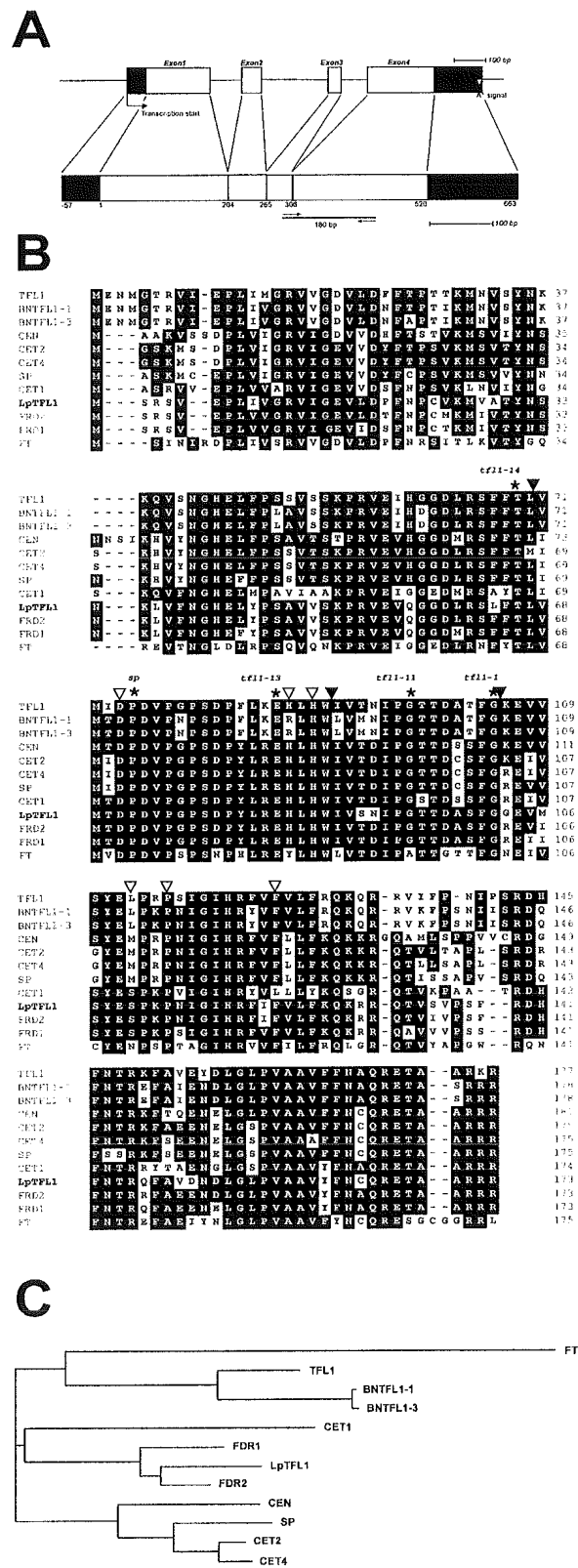
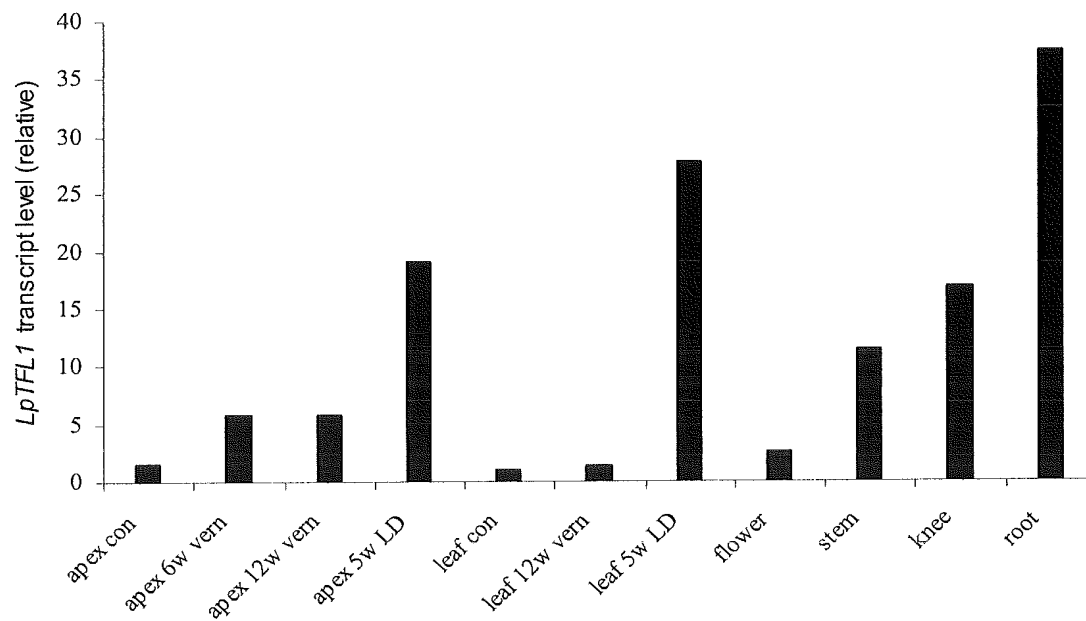


FIGURE 6

REPLACEMENT SHEET

FIGURE 7

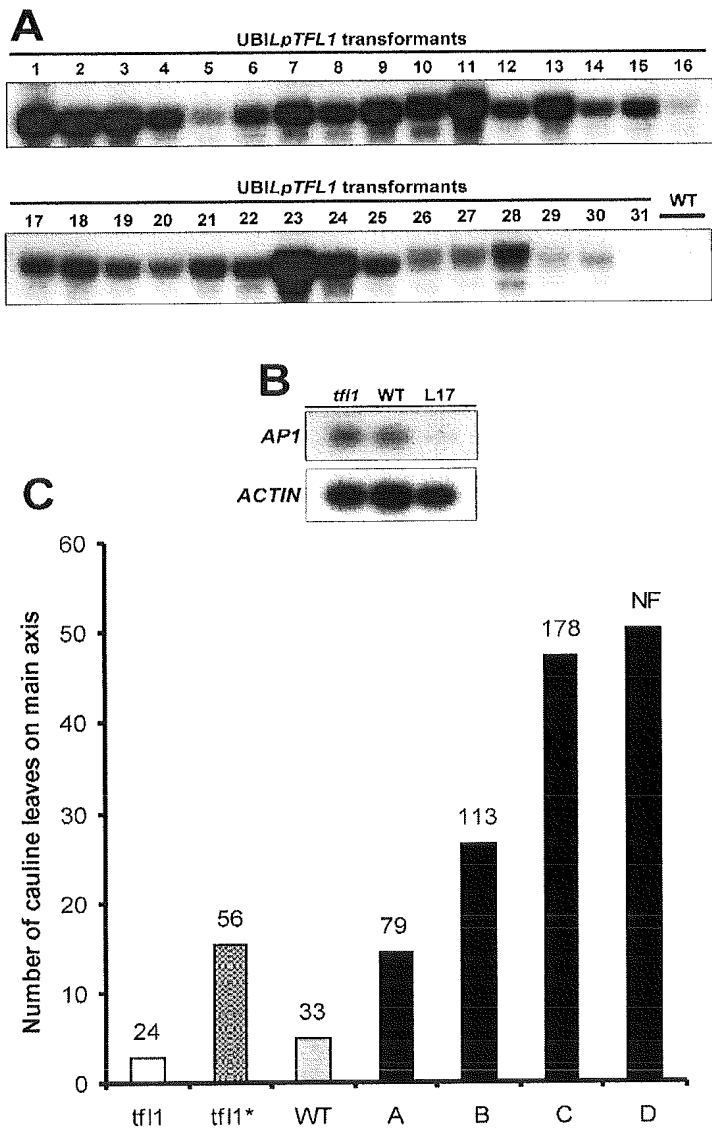
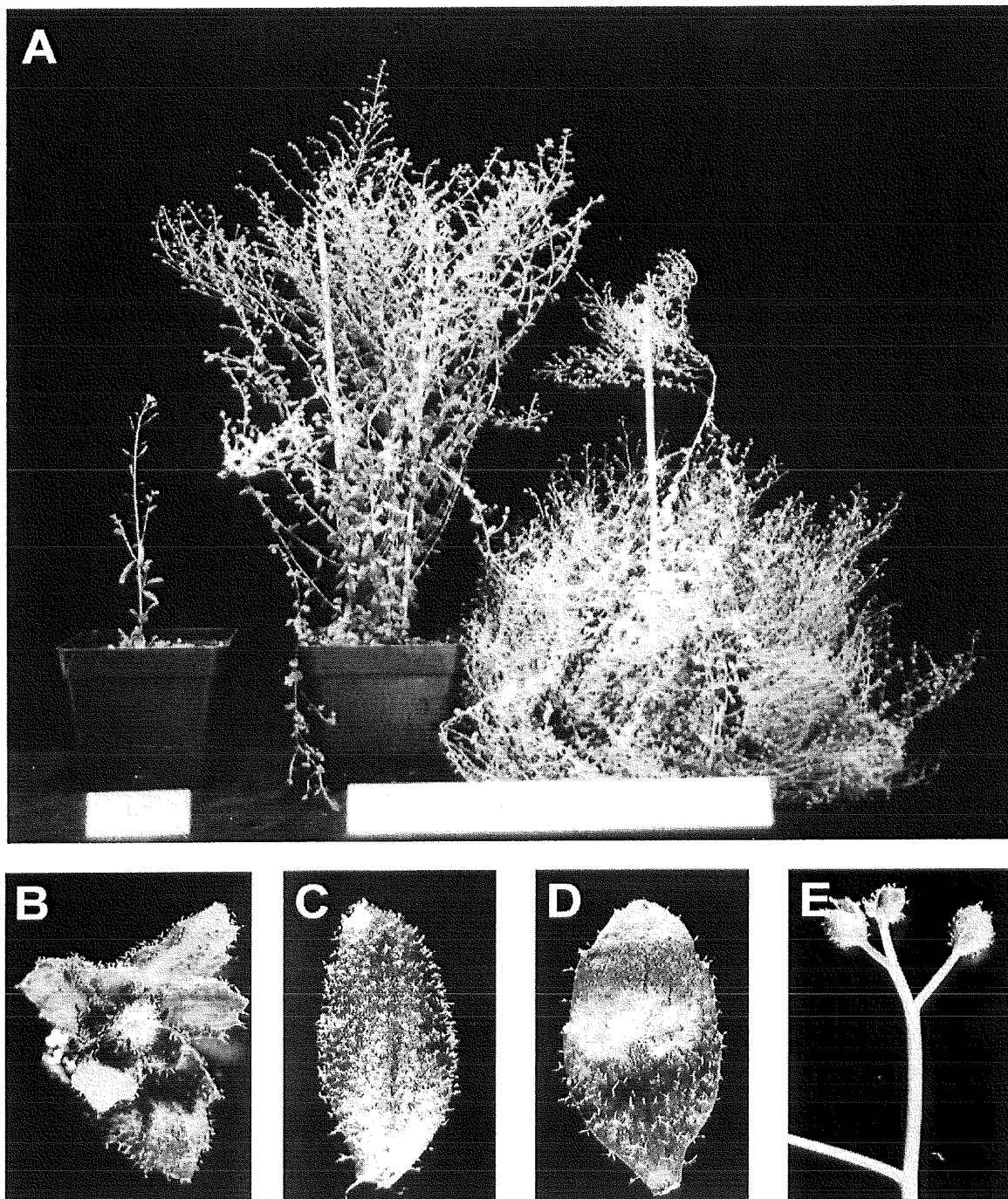
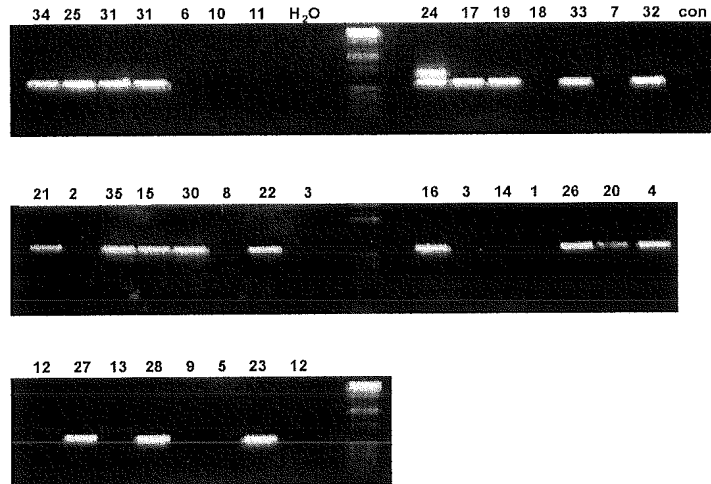


FIGURE 8



REPLACEMENT SHEET

FIGURE 9



REPLACEMENT SHEET

App No.: 10/507,355
Inventor: Klaus K. NIELSEN et al.
Title: METHOD OF REPRESSING FLOWERING IN A PLANT
REPLACEMENT SHEET

Docket No.: 0147-0262PUS1

Sheet 10 of 15 10/15

FIGURE 10

REPLACEMENT SHEET

FIGURE 11

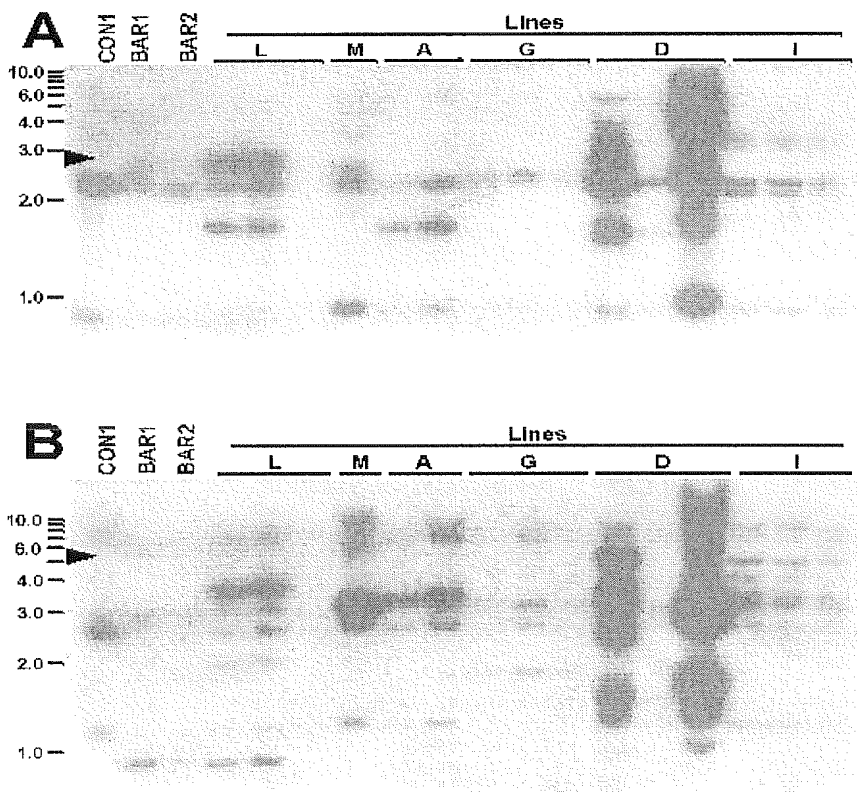


FIGURE 12

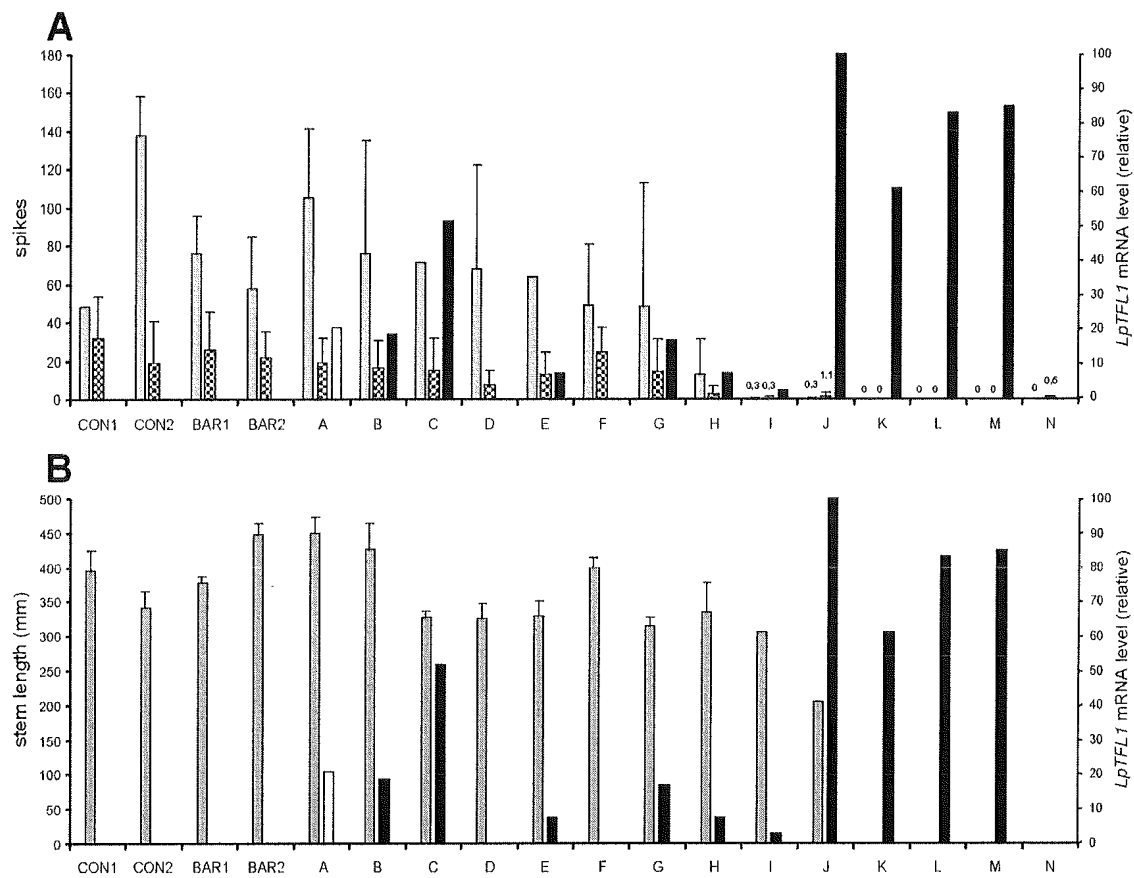


FIGURE 13

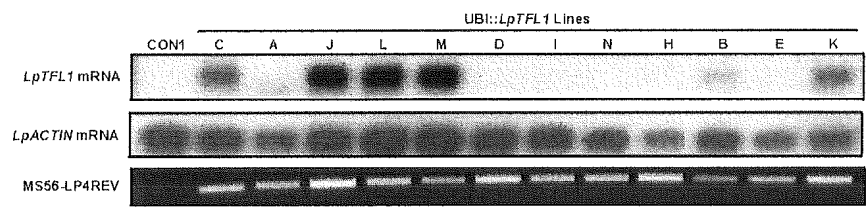


FIGURE 14

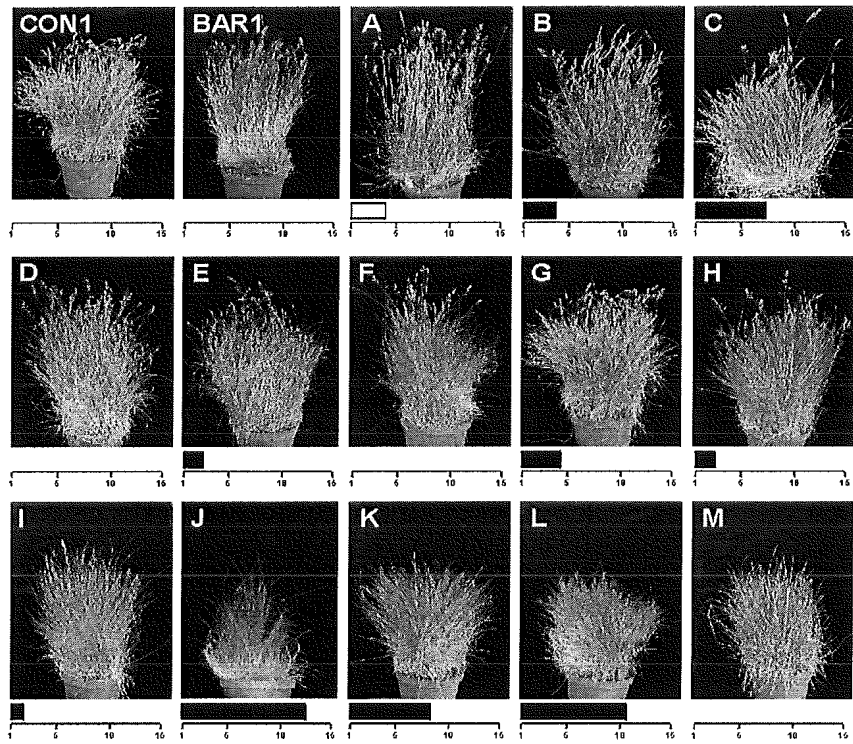


FIGURE 15

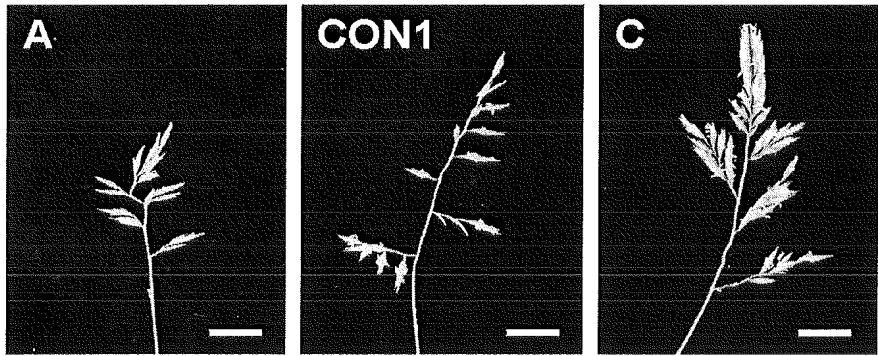


FIGURE 16: *Transformation Efficiency and Floral Activity of the Transformants*

Cultivar	Line No.	Inflorescences	PCR	RT-PCR
F6	CON	8	-	-
F6	7	18	-	-
F6	8	11	-	-
F6	17	5,3	+	-
F6	18	13,3	+	-
F6	24	12	+	+
F6	29	0	+	+
F6	32	0	+	+
F6	33	4	+	+
F6	36	0	+	+
ACTION	2	1,8	-	-
ACTION	5	3	-	-
ACTION	9	0,3	-	-
ACTION	12	2	-	-
ACTION	13	0	-	-
ACTION	16	0	+	-
ACTION	19	7,3	+	-
ACTION	21	4	+	+
ACTION	22	0,3	+	+
ACTION	23	0	+	+
ACTION	25	0,3	+	+
ACTION	27	0	+	+
ACTION	28	4	+	+
ACTION	31	0	+	+
ACTION	34	0	+	+
ACTION	35	0	+	+
TELSTAR	1	10	-	-
TELSTAR	3	1	-	-
TELSTAR	4	11,6	-	-
TELSTAR	6	10,8	-	-
TELSTAR	10	5	-	-
TELSTAR	11	3,8	-	-
TELSTAR	14	0	-	-
TELSTAR	15	3,8	+	-
TELSTAR	20	3,5	+	-
TELSTAR	26	0	+	+
TELSTAR	30	3,7	+	+

15/15

Figur 17: Transgene integration analysis by PCR using different primer combinations

Primer combination	UBI::LpTFL1 transgenic lines ^a															
	CASSETTE	CON	BAR	A	B	C	D	E	F	G	H	I	J	K	L	M
	UBI promoter H LpTFL1 intron HE															
MS33-LP575							0.8						+		+	0.8
MS33-LP4REV							0.55						+		+	0.55
MS31-LP4REV				+						1.4	+		+		+	1.5
MS56-LP575					+	+	+0.5	+		+0.5	+	+	+	+	+	+0.5
LP0-MS8					+	+	+M	+		+	+	+1.8	+	+	+	+1.6
MS56-LP4REV (intron::LpTFL1 probe)				+	+	+	+	+	+	+	+	+	+	+	+	+
				short			TATA box			short	short		ok		ok	TATA box
Result				ok			ok			ok	ok		ok		ok	ok
				truncated	ok	ok	ok + extra	ok	truncated	ok	ok	ok + extra	ok	ok	ok	ok + extra
LpTFL1 cDNA																

^aplus indicates that the observed fragment had the expected size, whereas numbers indicate that the fragment size deviated from the expected size (numbers in bold), blank field indicates that no PCR-product was detected; E, EcoRI; H, HindIII